

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Shah, Purvi

(ii) TITLE OF THE INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0256 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: Consensus
 (B) CLONE: 2122022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
 1 5 10 15
 Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu
 20 25 30
 Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
 35 40 45
 Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys
 50 55 60
 Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys
 65 70 75 80
 Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
 85 90 95
 Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
 100 105 110
 Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
 115 120 125
 Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
 130 135 140
 Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
 145 150 155 160
 Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
 165 170 175
 Glu Asp Gln Thr Lys Xaa Val Leu Xaa Tyr Tyr Gln Lys Lys Gly Val
 180 185 190
 Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val
 195 200 205
 Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser
 210 215 220
 Val Thr Pro
 225

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 854 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: Consensus
 (B) CLONE: 2122022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCANGCCA AAGCCCTGGT ACCCGCGCGG TGGGGCCTCA GTCTGCGGCC ATGGGGCGT	60
CCGCGCGGCT GCTGCGAGCG GTGATCATGG GGGCCCCGGG CTCGGGCAAG GGCACCGTGT	120
CGTCGCGCAT CACTACACAC TTTCGAGCTGA AGCACCTCTC CAGCGGGGAC CTGCTCCGGG	180

ACAAACATGCT	GCGGGGCACA	GAAATTGGCG	TGTTAGCCAA	GGCTTCATT	GACCAAGGGA	240
AACTCATCCC	AGATGATGTC	ATGACTCGGC	TGGCCCTTCA	TGAGCTGAAA	AATCTCACCC	300
AGTATAGCTG	GCTGTTGGAT	GGTTTCCAA	GGACACTTCC	ACAGGCAGAA	GCCCTAGATA	360
GAGCTTATCA	GATCGACACA	GTGATTAACC	TGAATGTGCC	CTTGAGGTC	ATTAAACAAAC	420
GCCTTACTGC	TCGCTGGATT	CATCCCCCA	GTGGCCGAGT	CTATAACATT	GAATTCAACC	480
CTCCCAAAAC	TGTGGCATT	GATGACCTGA	CTGGGGAGCC	TCTCATTCAAG	CGTGAGGATG	540
ATAAACACAGA	GACGGTTATC	AAGAGACTAA	AGGCTTATGA	AGACCAAACA	AAGNCAGTCC	600
TGGNATATTA	CCAGAAAAAA	GGGGTGTG	AAACATTCTC	CGGAACAGAA	ACCAACAAGA	660
TTTGGCCCTA	TGTATATGCT	TTCCCTACAAA	CTAAAGTTCC	ACAAAGAAGC	CAGAAAGCTT	720
CAGTTACTCC	ATGAGGAGAA	ATGTGTGAA	CTATTAATAG	TAAGATGGC	AAACCTCCTA	780
GTCCTTGCAT	TTAGAAGCTG	CTTTCTCAA	GACTTCTAGT	ATGTATGAAT	TCTTGAAAAA	840
TTATATTACT	TTTA					854

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 217576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Ala	Ser	Ala	Arg	Leu	Leu	Arg	Ala	Ala	Ile	Met	Gly	Ala	Pro
1		5				10					15				
Gly	Ser	Gly	Lys	Gly	Thr	Val	Ser	Ser	Arg	Ile	Thr	Lys	His	Phe	Glu
			20			25					30				
Leu	Lys	His	Leu	Ser	Ser	Gly	Asp	Leu	Leu	Arg	Asp	Asn	Met	Leu	Arg
	35					40				45					
Gly	Thr	Glu	Ile	Gly	Val	Leu	Ala	Lys	Thr	Phe	Ile	Asp	Gln	Gly	Lys
	50				55			60							
Leu	Ile	Pro	Asp	Asp	Val	Met	Thr	Arg	Leu	Val	Leu	His	Glu	Leu	Lys
65					70				75			80			
Asn	Leu	Thr	Gln	Tyr	Asn	Trp	Leu	Leu	Asp	Gly	Phe	Pro	Arg	Thr	Leu
			85					90				95			
Pro	Gln	Ala	Glu	Ala	Leu	Asp	Arg	Ala	Tyr	Gln	Ile	Asp	Thr	Val	Ile
	100					105				110					
Asn	Leu	Asn	Val	Pro	Phe	Glu	Val	Ile	Lys	Gln	Arg	Leu	Thr	Ala	Arg
	115					120			125						
Trp	Ile	His	Pro	Gly	Ser	Gly	Arg	Val	Tyr	Asn	Ile	Glu	Phe	Asn	Pro
130					135			140							
Pro	Lys	Thr	Met	Gly	Ile	Asp	Asp	Leu	Thr	Gly	Glu	Pro	Leu	Val	Gln
145						150			155			160			
Arg	Glu	Asp	Asp	Arg	Pro	Glu	Thr	Val	Val	Lys	Arg	Leu	Lys	Ala	Tyr
	165						170			175					
Glu	Ala	Gln	Thr	Glu	Pro	Val	Leu	Glu	Tyr	Tyr	Arg	Lys	Lys	Gly	Val
	180					185			190						
Leu	Glu	Thr	Phe	Ser	Gly	Thr	Glu	Thr	Asn	Lys	Ile	Trp	Pro	His	Val
195					200			205							
Tyr	Ala	Phe	Leu	Gln	Thr	Lys	Leu	Pro	Gln	Arg	Ser	Gln	Glu	Thr	Ser

210
Val Thr Pro
225

215

220

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 450312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Ser Gly Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
1 5 10 15
Gly Ser Gly Lys Gly Thr Gly Ser Ser Arg Ile Thr Lys His Phe Glu
20 25 30
Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Gln Asn Met Leu Gln
35 40 45
Gly Thr Glu Ile Ala Val Leu Ala Lys Ser Phe Ile Asp Gln Gly Lys
50 55 60
Leu Ile Pro Asp Asp Asp Met Thr Arg Leu Ala Leu His Glu Leu Lys
65 70 75 80
Asn Leu Thr Gln Cys Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
85 90 95
Pro Gln Ala Glu Ala Leu Asp Arg Val Tyr Gln Ile Asp Thr Val Ile
100 105 110
Asn Leu Asn Val Pro Phe Glu Val Ile Lys Leu Arg Leu Thr Ala Arg
115 120 125
Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
130 135 140
Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
145 150 155 160
Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
165 170 175
Glu Ala Gln Thr Glu Pro Val Leu Gln Tyr Tyr Gln Lys Lys Gly Val
180 185 190
Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Arg Pro His Val
195 200 205
Tyr Ser Phe Leu Gln Met Lys Val Pro Glu Thr Ile Gln Lys Ala Ser
210 215 220
Val Thr Pro
225

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 28577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ser Lys Leu Leu Arg Ala Val Ile Leu Gly Pro Pro Gly Ser
1 5 10 15
Gly Lys Gly Thr Val Cys Gln Arg Ile Ala Gln Asn Phe Gly Leu Gln
20 25 30
His Leu Ser Ser Gly His Phe Leu Arg Glu Asn Ile Lys Ala Ser Thr
35 40 45
Glu Val Gly Glu Met Ala Lys Gln Tyr Ile Glu Lys Ser Leu Leu Val
50 55 60
Pro Asp His Val Ile Thr Arg Leu Met Met Ser Glu Leu Glu Asn Arg
65 70 75 80
Arg Gly Gln His Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu Gly Gln
85 90 95
Ala Glu Ala Leu Asp Lys Ile Cys Glu Val Asp Leu Val Ile Ser Leu
100 105 110
Asn Ile Pro Phe Glu Thr Leu Lys Asp Arg Leu Ser Arg Arg Trp Ile
115 120 125
His Pro Pro Ser Gly Arg Val Tyr Asn Leu Asp Phe Asn Pro Pro His
130 135 140
Val His Gly Ile Asp Asp Val Thr Gly Glu Pro Leu Val Gln Gln Glu
145 150 155 160
Asp Asp Lys Pro Glu Ala Val Ala Ala Arg Leu Arg Gln Tyr Lys Asp
165 170 175
Val Ala Lys Pro Val Ile Glu Leu Tyr Lys Ser Arg Gly Val Leu His
180 185 190
Gln Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val Tyr Thr
195 200 205
Leu Phe Ser Asn Lys Ile Thr Pro Ile Gln Ser Lys Glu Ala Tyr
210 215 220